Marker-free Method for Reconstruction of Human Motion Trajectories

Jaroslav Majernik[*]

Department of Medical Informatics, Faculty of Medicine, Pavol Jozef Safarik University in Kosice
Trieda SNP 1, Kosice, Slovak Republic

[*]jaroslav.majernik@upjs.sk

Abstract

Digital image processing techniques were used to develop algorithms for automatic detection of human motion trajectories in this study. Based on these algorithms, the marker-free analysis system has been developed and tested in analysis of human gait. Experiments have been made on a group of ten healthy male subjects whose walking was captured by standard camera. Here, only the movements of lower limbs' anatomical landmarks in sagittal plane were considered. Trajectories of hip, knee, ankle and fifth metatarsal head were reconstructed by this new system and used to calculate anatomical joint angles and spatio-temporal parameters. To assess the accuracy of the method, the real distances were measured by laboratory measuring-tape and compared with those reconstructed by the system. The average difference between the reconstructed and measured values was 3.83 mm with standard deviation 0.69 mm. Kinematical parameters were also compared with those obtained by commercial marker-based motion capture system SMART with no statistically significant differences. The laboratory tests shows satisfying results and the proposed method might be applicable to kinematical analysis of human motion.

Keywords

Motion Trajectories; Gait Analysis; Anatomical Joint Angles

Introduction

To analyse kinematics of human motion, it is necessary to track motion of individual body segments and/or motion of anatomical joints. In general, there are two main approaches to examine motion activities. First approach is known as subjective or qualitative and it is based on visual observation of appropriate movement, e.g. when the clinician examines his/her patient. Its disadvantage is that the identical deviations from normal motion patterns can be classified once as irrelevant and another time as serious, depending on clinician's subjective opinion. The other approach is objective or also termed as quantitative and it is based on various measurement methods and techniques. Here, a lot of evaluation processes and appropriate measurement devices were developed during the history of motion analysis all around the world. Most of the systems, used to capture dynamical tasks, are based on tracking of small either passive or active markers attached to the surface of analysed objects or subjects. In clinical trials, the markers are attached on particular anatomical landmarks of the patients' bodies according to the specific marker sets. Although these laboratory systems using sophisticated methods, at the very high technological level, are accurate and can be easily operated, there are still efforts to develop less expensive and even more available systems. Such systems the researchers work on, are based on artificial intelligence and/or digital image processing techniques, where the motion is tracked without the use of any markers or special apparel. These systems also termed as "marker-less" or "marker-free" are developed with the aim to have sufficient accuracy and to be easily operated. Many laboratories work on various methodologies including wearing of special clothing, using of black or highly contrasted backgrounds, complicated edge detection algorithms, background elimination, video-frames processing etc. We created algorithms for motion analysis system that will be able to reconstruct human motion trajectories from standard videorecords without necessity to use any special clothing or contrast background as well as without the need to make any arrangements in video frames. The system was tested to analyse kinematical data in sagittal plane as we processed the data obtained by single camera. However, using the combination of motion trajectories from different views might produce 3D analysis.

Videosignal Processing

The main principle of the proposed method is based on assumption that the digital videorecords are spatio-temporal digitized signals. In this case, the temporal digitizing results in finite number of recorded frames and spatial digitizing define the finite number of

picture elements in the frame. Both the temporal and the spatial digitizing should offer sufficient view on moving subject during the whole analysed movement, e.g. at least one complete gait cycle in gait analysis. Then, the dynamic discrete image will be defined by discrete luminance function (1).

$$l'(x, y, t) = \varphi(x, y, t)l(x, y, t) \tag{1}$$

Where $\varphi(x,y,t)$ is digitizing function and $l(x,y,t)$ is continuous luminance function of dynamic continuous image. Such spatio-temporal digitizing of continuous image signal is shown in FIG.1.
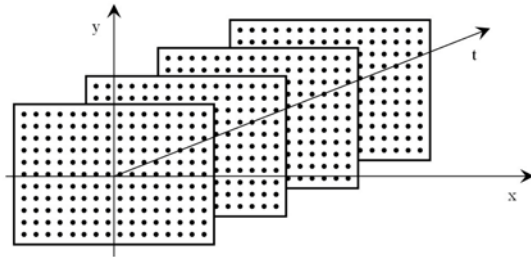

FIG. 1 DISCRETE IMAGE SIGNAL

The point of interests, i.e. the point of which movement should be tracked in the sequence of frames can be presented by one picture element or by the group of picture elements. Naturally, there can be a lot of similar or even equal picture elements in single frame, so the tracked areas will be specified by several adjacent picture elements rather than by single picture element.

We decided to use anatomical joints of lower limb as our reference points for kinematical gait analysis in sagittal plane, where the model of lower limb is presented by three segments (thigh, calf, foot) and by four points (hip, knee, ankle and fifth metatarsal head). These four points need to be specified in all frames of the motion sequence to get their trajectories. Even if it is possible to use various shapes to define particular point (anatomical joint), we use square blocks of picture elements. It is because of the speed in calculations and far from better results we obtained using circular, triangle or other freely drawn shapes while testing the new method.

Anatomical joint is then specified by the matrix $\underline{J}$ of picture elements $a_{i,j}$ in particular frame as it is stated in formula (2).

$$\underline{J} = \begin{pmatrix} a_{1,1} & a_{1,2} & a_{1,3} & \dots & a_{1,K-1} & a_{1,K} \\ a_{2,1} & a_{2,2} & a_{2,3} & \dots & a_{2,K-1} & a_{2,K} \\ \dots & & & & & \dots \\ a_{K-1,1} & a_{K-1,2} & a_{K-1,3} & \dots & a_{K-1,K-1} & a_{K-1,K} \\ a_{K,1} & a_{K,2} & a_{K,3} & \dots & a_{K,K-1} & a_{K,K} \end{pmatrix} \tag{2}$$

Here, K specifies the size of the square matrix and the centre point of particular anatomical joint is specified as single centred picture element $A(x,y)$ given by the following formula (3).

$$A(x, y) = a_{\frac{K+1}{2}, \frac{K+1}{2}} \tag{3}$$

If the value K is small, then the reconstruction process is faster, but the accuracy might be worsen. Otherwise, the values of several tenths of picture elements will significantly increase the reconstruction time. Our tests showed the values from 7 to 11 are optimal. An example of ankle joint specification is shown in FIG.2.

FIG. 2 ANKLE JOINT SPECIFIED FOR K = 5, 7, 9, 11, 13 AND 15

Individual frames can be processed as black and white or as colour. In the case we use RGB frames, the values of all three colours are included in calculations and the elements of the matrix (2) are presented as arrays with the size of 1x3.

$$a_{1,1} = [R_{1,1}, G_{1,1}, B_{1,1}]$$
$$a_{1,2} = [R_{1,2}, G_{1,2}, B_{1,2}] \tag{4}$$
$$\dots$$
$$a_{K,K} = [R_{K,K}, G_{K,K}, B_{K,K}]$$

The distance between two picture elements, eventually between two anatomical joints, e.g. knee $K(x_k, y_k)$ and ankle $A(x_a, y_a)$ (see FIG.3) in particular frame will be calculated as Euclidean distance D_E according to the formula (5).

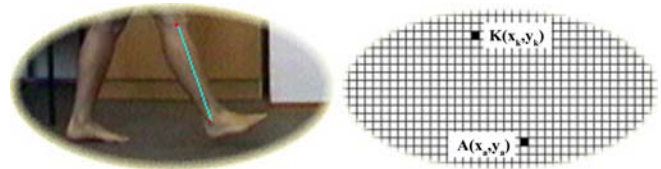$$D_E = \sqrt{(x_k - x_a)^2 + (y_k - y_a)^2} \tag{5}$$

FIG. 3 EUCLIDEAN DISTANCE BETWEEN KNEE AND ANKLE

Having positions of all points of the model, defined in appropriate frame, it is also possible to calculate anatomical joint angles of the sagittal plane, i.e. hip flexion/extension, knee flexion/extension and ankle plantar/dorsal flexion. To calculate other kinematical parameters including velocities, accelerations and spatio-temporal parameters considering subject's anthropometry it is necessary to have positions of all

points in all frames of the motion activity videorecord. A designed motion tracking algorithm will be used to get them automatically.

Motion Tracking Algorithm

Movement of individual body segment in sagittal plane between two consecutive frames may be caused by its displacement and/or by its rotation. In that case, the position of particular point with coordinates (x,y) in the frame F will be changed to position (x',y') in the next frame $F+1$ as defined in formula (6).

$$\begin{pmatrix} x' \\ y' \end{pmatrix} = \begin{pmatrix} x \\ y \end{pmatrix} + \begin{pmatrix} \Delta x \\ \Delta y \end{pmatrix} \tag{6}$$

Where Δx is displacement in direction of x axis and Δy is displacement in direction of y axis. Detection of these displacements is based on inter-frame prediction with motion compensation. Here, the point's motion between two consecutive frames is defined by vector of motion. The efficiency of motion inter-frame prediction depends on accuracy of vector of motion estimation.

Designed vector of motion estimation uses correlation characteristics of motion pictures. Here, the blocks of pixels, defining individual points of used model (hip, knee, ankle and fifth metatarsal head), are compared with blocks of picture elements taken from the next consecutive frame. All compared blocks have to be the same size. However, this size may vary during tracking process if necessary. The correlation maximum of two blocks of pixels defines vector of motion of particular joint, and the correlation of two blocks of picture elements is calculated as given by the formula (7).

$$r(i,j) = \frac{\sum_{m=1}^{K} \sum_{n=1}^{K} J_F(m,n) J_{F+1}(m+i,n+j)}{\left[\sum_{m=1}^{K} \sum_{n=1}^{K} J_F^2(m,n)\right]^{\frac{1}{2}} \left[\sum_{m=1}^{K} \sum_{n=1}^{K} J_{F+1}^2(m+i,n+j)\right]^{\frac{1}{2}}} \tag{7}$$

Where $J_F(m,n)$ and $J_{F+1}(m,n)$ are values of picture elements in current frame F and next frame $F+1$, m and n are coordinates of picture element in particular block of picture elements.

To make tracking process faster, the number of calculations was decreased by selection of small scanning area (SA), in which the new position of particular joint is expected. It is more efficient than to search for the correlation maximum in whole frame. The size of scanning area depends on motion speed, frame rate of used camera and may vary during

tracking as well. The scanning area, located in the next frame $(F+1)$ and used to search for vector of motion (V) of block of picture elements (KxK) from current frame (F) is shown in FIG.4 .
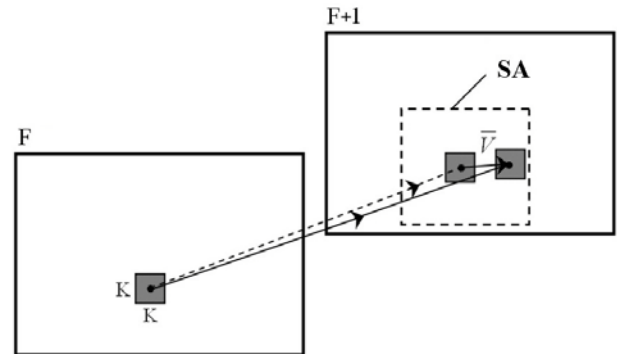

FIG. 4 USING OF SEARCHING AREA DECREASES NUMBER OF CALCULATIONS

Vector of motion of two blocks of picture elements from two consecutive frames is then given by the correlation maximum, and is located in the scanning area. This is described by the formula (8),

$$\overline{V} = \left\{ (\hat{i}, \hat{j}) : r(\hat{i}, \hat{j}) \geq r(i,j); \forall i, j \in SA \right\} \tag{8}$$

where SA is limited by maximal displacement d_m of block of picture element as determined in formula (9).

$$\begin{aligned} -d_m \leq i \leq d_m \\ -d_m \leq j \leq d_m \end{aligned} \tag{9}$$

Basicaly, we use SA of the size SxS picture elements, where S is whole number equal to $K+2d_m$. An example of SA is shown in FIG.5.
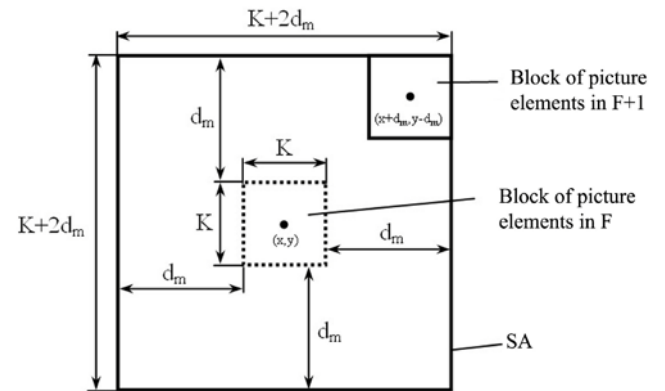

FIG. 5 SEARCHING AREA OF THE FRAME F+1

Centre of SA is given by coordinates of picture element (x,y) that specifies centre of particular anatomical joint in current frame F. Thus, all possible directions of movement in the frame $F+1$ are covered and there is no need to specify direction of motion. Doing this, the trajectories reconstruction process can be fully automated.

Searching of correlation maximum of all interested points continues frame by frame in whole videorecord. Tracking procedure is stopped at the end of frame sequence or it can be stopped earlier by the operator if there is a need to check already reconstructed trajectories. The diagram of designed motion tracking algorithm is shown in FIG.6.
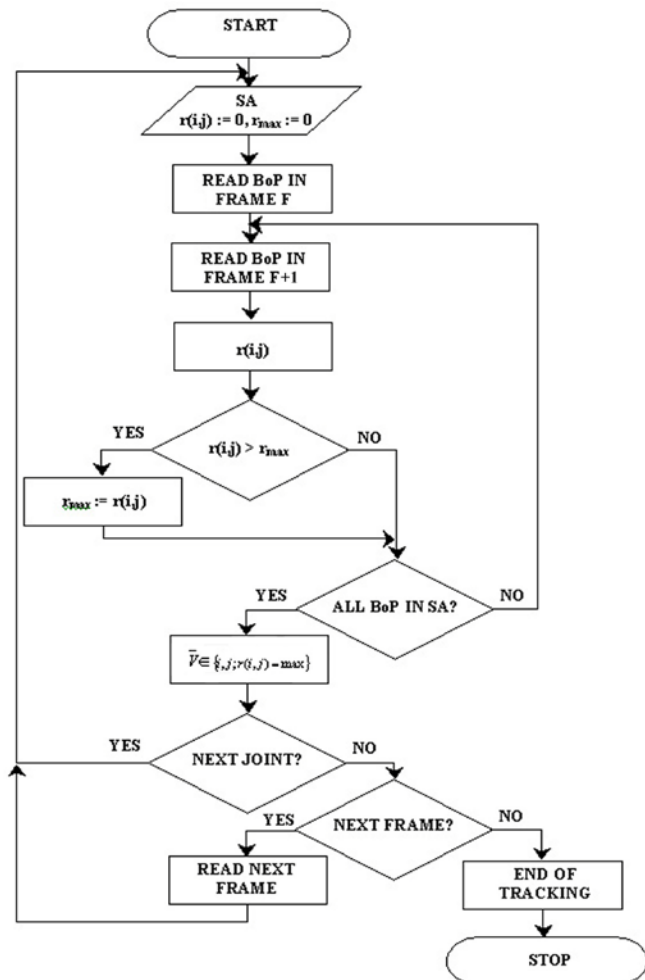

FIG. 6 AUTOMATIC MOTION TRACKING ALGORITHM

Laboratory Experiments and Results

All designed algorithms were integrated in motion analysis system and tested on the group of ten young healthy adult male subjects in the average age of 24.8 years (SD 2.18) and average height 178.54 cm (SD 5.4). The subjects had no known pathology and they were asked to walk at their natural speed during the laboratory tests.

Gait in sagittal plane was captured as first and then the trajectories of all lower extremity joints were reconstructed. All the patients were recorded five times and there were no statistically significant differences between these individually reconstructed

trajectories (p 0.05). To visualise motion trajectories during and after motion tracking procedure a stick figure was used. An example of stick figure and reconstructed motion trajectories of individual joints and body segments is shown in FIG.7.
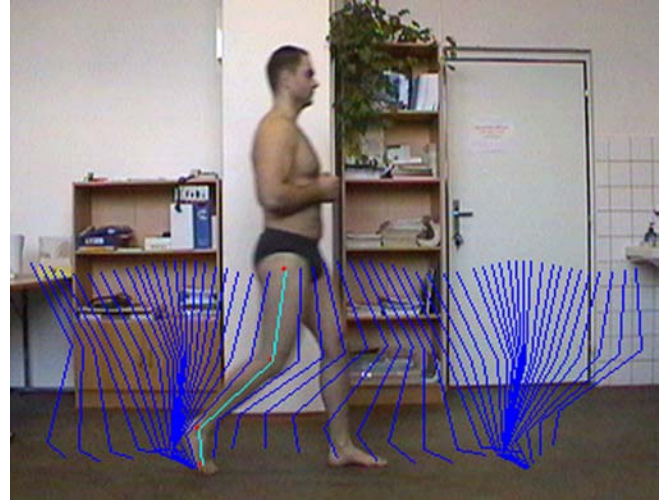

FIG. 7 STICK FIGURE GENERATED FROM RECONSTRUCTED TRAJECTORIES

The following parameters were analysed in all subjects:

- trajectories of motion – positions, velocities and accelerations of individual joints,

- anatomical joint angles – hip flexion/extension, knee flexion/extension, and ankle plantar/dorsal flexion,

- spatio-temporal parameters – gait cycle length, gait cycle time, gait cycle velocity, cadence (cycles per minute), stance phase and swing phase.

To verify validity of these parameters, all the subjects were analysed also by the commercial six cameras optical motion analysis system SMART (BTS, Padova). Sagittal plane data from this marker-based system were compared with these obtained by our method and there were confirmed no statistically significant differences at the significance level of 0.05.

The data of these healthy subjects were also used to create normative gait database, which is usually used by gait laboratories in clinical trials to identify pathologies in patients with motion disorders. Here, the anatomical joint angles were standardised to one gait cycle, where the data of all subjects were defined in identical points of gait cycle. Cubic spline interpolation was used in all angles and for all included subject to do it. Definition of normative gait data was made by determination of upper and lower

bounds of reliability interval. As for the references in literature and the most used values in mathematical statistics and laboratories we used the probability of 95% reliability interval coverage. This interval means that the data included in are the data of normal healthy subjects and the data out of this interval represent certain type of pathological pattern in subject's gait. FIG.8 shows this normative gait database of three anatomical joint angles (hip flexion/extension, knee flexion/extension and ankle plantar/dorsal flexion angles).
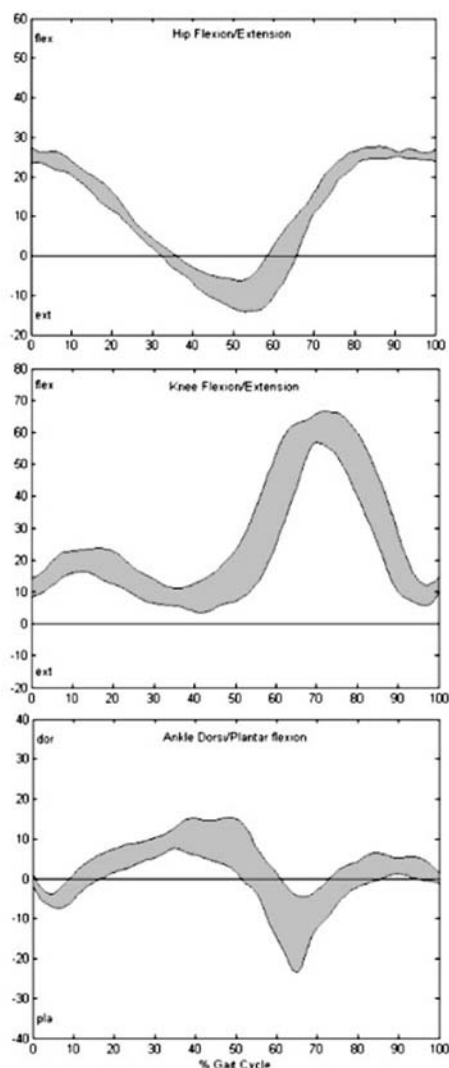

FIG. 8 NORMATIVE GAIT DATABASE OF ANATOMICAL JOINT ANGLES IN SAGITTAL PLANE

Acquired normative gait database can be easily updated with the data of any new analysed healthy subject.

Conclusions

Newly developed marker-free analysis method was described in this paper. The algorithms were implemented into the motion analysis system, whose functionalities were verified at the group of young healthy male subjects. Here, the trajectories of motion, and kinematics parameters were acquired and normative gait database was generated.

The experimental results convinced us that the designed methodology and the designed system are clinically applicable and are not limited to only laboratory usage. Determination of normative gait database might help to utilize the system in the process of pathological gait assessment.

ACKNOWLEDGMENT

REFERENCES

Alkjaer T., Simonsen E.B., Dyhre-Poulsen P.: "Comparison of inverse dynamics calculated by two- and three-dimensional models during walking", Gait and Posture 13, 2001, 73-77.

Assi A., Ghanem I., Laassel E.M., Penneçot G.F., Lavaste F., Skalli W.: "Normalcy gait index and kinematics: Uncertainty and repeatability on healthy children database: Preliminary application on cerebral palsy group", Gait & Posture, Volume 24, Supplement 2, December 2006, Pages S49-S50.

Blanc Y., Balmer C., Landis T., Vingerhoets F.: "Temporal parameters and patterns of the foot roll over during walking: normative data for healthy adults", Gait and Posture 10, 1999, 97-108

Chaudhari A.M., Bagg R.W., Alexander E.J., Andriacchi T.P.: "A video based, markerless motion tracking system for biomechanical analysis in arbitrary environment", BED-Vol. 50, 2001 Bioengineering Conference, ASME 2001

Hof L.: "Scaling gait data to body size", Gait and Posture, Volume 4, 1996, 222-223.

Kobayashi K., Gransberg L., Knutsson E., Nolén P.: "A new system for three-dimensional gait recording using electromagnetic tracking", Gait and Posture 6, 1997, 63-75.

Lakany H.M.: "A generic kinematic pattern for human walking", Neurocomputing 35, 2000, 27-54.

Leardini A., Benedetti M.G., Catani F., Simoncini L., Giannini S.: "An anatomically based protocol for the description of foot segment kinematics during gait", Clinical Biomechanics 14, 1999, 528-536.

Li E.B., Tieu A.K., yuen W.Y.D.: "Application of digital image correlation technique to dynamic measurement of the velocity field in the deformation zone in cold rolling", Optics and Lasers in Engineering, Volume 39, 2003, 479-488.

Majerník J. at all.: "Some Clinical Studies of Human Movement at the Rehabilitation Clinic", 12th Annual Meeting, ESMAC 2003, Marseille, France.

Macurova A., Macura D.: "Asymptotic properties of the variables of the roughness surface", Applied Surface Science, DOI: 10.1016/j.apsusc.2012.10.086.

McClelland Jodie A., Webster Kate E., Grant Cameron, Feller Julian, "Alternative modelling procedures for pelvic marker occlusion during motion analysis", Gait & Posture 31 (2010) pp. 415–419.

Ounpuu S., Davis R.B., DeLuca P.A.: "Joint kinetics: methods, interpretation and treatment decision-making in children with cerebral palsy and myelomeningocele", Gait and Posture 4, 1996, 62-78.

Pediaditis Matthew, Tsiknakis Manolis, Leitgeb Norbert: "Vision-based motion detection, analysis and recognition of epileptic seizures—A systematic review", Computer methods and programs in biomedicine 108 (2012) pp. 1133–1148.

Penhaker, M., Krejcar, O., Kasik, V., Snášel, V.: "Cloud computing environments for biomedical data services", Lecture Notes in Computer Science, Volume 7435 LNCS, 2012, Pages 336-343, DOI: 10.1007/978-3-642-32639-4_41.

Persson T.: "A marker-free method for tracking human lower limb segments based on model matching", International Journal of Bio-Medical Computing 41 (1996) pp. 87-97.

Reid I., Davison A., Deutscher J.: "Markerless visual capture of complex full-body motion", University of Oxford, 2002.

Šimšík D., Galajdová A., Majerník J., Želinský Ľ.: "Contribution to investigation of pre-surgical rehabilitation effectiveness for total hip endoprostheses patients", International Journal of Rehabilitation Research, Volume 27, 2004, ISSN 0342-5282, Ljubljana, Slovenia, pp. 87 – 87.

Šimšík D., Majerník J., Galajdová A.: The investigation of patient mobility using motion analysis. Mechanika w medycynie 7. ISSN 1427-0374, Rzeszow, Poland, 2004. pp. 223 - 229.

Zanchi V., Papić V., Cecić M.: "Quantitative human gait analysis", Simulation Practice and Theory 8, 2000, pp. 127-139.

Zelmana Ido, Galuna Meirav, Akselrod-Ballina Ayelet, Yekutieli Yoram, Hochnerb Binyamin, Flash Tamar: "Nearly automatic motion capture system for tracking octopus arm movements in 3D space", Journal of Neuroscience Methods 182 (2009) pp. 97–109.

Živčák, J., Hudák, R., Tóth, T.: Rat skin wounds tensile strength measurements in the process of healing. IEEE 10th Jubilee International Symposium on Applied Machine Intelligence and Informatics, SAMI 2012 – Proceedings 2012, Article number 6208996, Pages 389-392.

Jaroslav MAJERNIK was born in Presov, Slovakia in 1977. He received his Master's degree in the field of electronics and telecommunications at Technical University in Kosice, Slovakia in 2000 and Ph.D. degree in bionics and biomechanics in 2005. His professional and research interests include biomedical engineering and medical informatics. He is author or co-author of seven books and more than 130 research works and projects in the fields of biomechanics and computer science. Currently, he acts as assistant professor and the head of Department of Medical Informatics at the Faculty of Medicine, Pavol Jozef Safarik University in Kosice, Slovakia. Dr. Majernik is a member of ESMAC, MEFANET Coordination Council and several national societies.